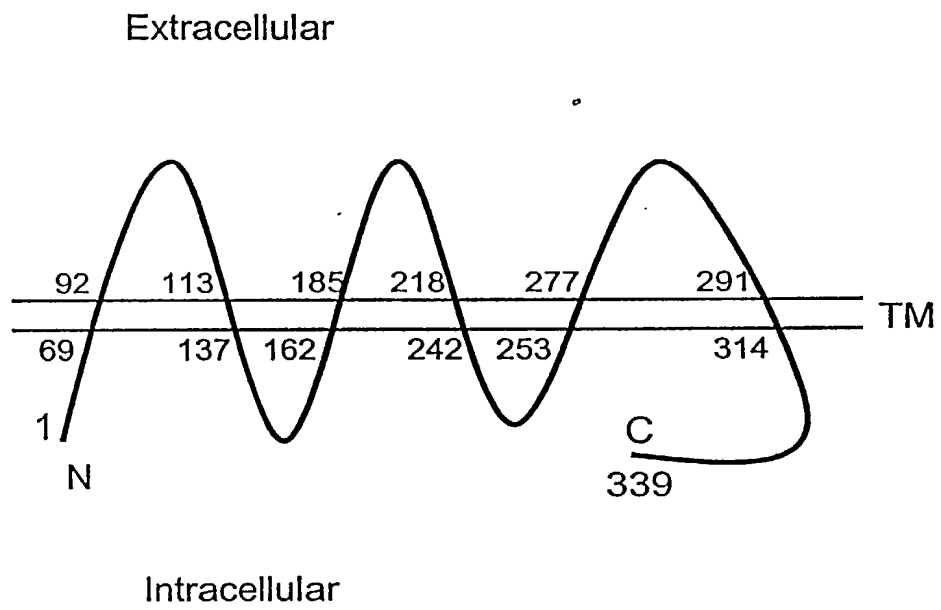


FIG. 1A

	(SEQ ID NO:1)	GAG	ACT	CAC	GGT	CAA	GCT	AAG	GCG	AAG	AGT	GGG	TGG	CTG	AAG	CCA	TAC	TAT	TTT	ATA	GAA
(SEQ ID NO:2)	M	E	S	R	K	D	I	T	N	Q	E	E	L	W	K	M	K	P	R		
61	TTA	ATG	GAA	AGC	AGA	AAA	GAC	ATC	ACA	AAC	CAA	GAA	GAA	CTT	TGG	AAA	ATG	AAG	CCT	AGG	
	R	N	L	E	E	D	D	Y	L	H	K	D	T	G	E	T	S	M	L	K	
121	AGA	AAT	TTA	GAA	GAA	GAC	GAT	TAT	TTG	CAT	AAG	GAC	ACG	GGA	GAG	ACC	AGC	ATG	CTA	AAA	
	R	P	V	L	L	H	L	H	Q	T	A	H	A	D	E	F	D	C	P	S	
181	AGA	CCT	GTG	CTT	TTG	CAT	TTG	CAC	CAA	ACA	GCC	CAT	GCT	GAT	GAA	TTT	GAC	TGC	CCT	TCA	
	E	L	Q	H	T	Q	E	L	F	P	Q	W	H	L	P	I	K	I	A	A	
241	GAA	CTT	CAG	CAC	ACA	CAG	GAA	CTC	TTT	CCA	CAG	TGG	CAC	TTG	CCA	ATT	AAA	ATA	GCT	GCT	
	I	I	A	S	L	T	F	L	Y	T	L	L	L	E	V	I	H	P	L	A	
301	ATT	ATA	GCA	TCT	CTG	ACT	TTT	CTT	TAC	ACT	CTT	CTG	AGG	GAA	GTA	ATT	CAC	CCT	TTA	GCA	
	T	S	H	Q	Q	Y	F	Y	K	I	P	I	L	V	I	N	K	V	L	P	
361	ACT	TCC	CAT	CAA	CAA	TAT	TTT	TAT	AAA	ATT	CCA	ATC	CTG	GTC	ATC	AAC	AAA	GTC	TTG	CCA	
	M	V	S	I	T	L	L	A	L	V	Y	L	P	Q	V	I	A	A	I	V	
421	ATG	GTT	TCC	ATC	ACT	CTC	TTG	GCA	TTG	GTT	TAC	CTG	CCA	GGT	GTG	ATA	GCA	GCA	ATT	GTC	
	Q	L	H	N	G	T	K	Y	K	K	F	P	H	W	L	D	K	W	M	L	
481	CAA	CTT	CAT	AAT	GGA	ACC	AAG	TAT	AAG	AAG	TTT	CCA	CAT	TGG	TTG	GAT	AAG	TGG	ATG	TTA	
	T	R	K	Q	F	G	L	L	S	F	F	F	A	V	L	H	A	I	Y	S	
541	ACA	AGA	AAG	CAG	TTT	GGG	CTT	CTC	AGT	TTC	TTT	TTT	GCT	GTA	CTG	CAT	GCA	ATT	TAT	AGT	
	L	S	Y	P	M	R	R	S	Y	R	Y	K	L	L	N	W	A	Y	Q	Q	
601	CTG	TCT	TAC	CCA	ATG	AGG	CGA	TCC	TAC	AGA	TAC	AAG	TTG	CTA	AAC	TGG	GCA	TAT	CAA	CAG	
	V	Q	Q	N	K	E	D	A	W	I	E	H	D	V	W	R	M	E	I	Y	
661	GTC	CAA	CAA	AAT	AAA	GAA	GAT	GCC	TGA	ATT	GAG	CAT	GAT	GTT	TGG	AGA	ATG	GAG	ATT	TAT	
	V	S	L	G	I	V	G	L	A	I	L	A	L	L	A	V	T	S	I	P	
721	GTG	TCT	CTG	GGA	ATT	GTG	GGA	TTG	GCA	ATA	CTG	GCT	CTG	TTG	GCT	GTG	ACA	TCT	ATT	CCA	
	S	V	S	D	S	L	T	W	R	E	F	H	Y	I	Q	S	K	L	G	I	
781	TCT	GTG	AGT	GAC	TCT	TTG	ACA	TGG	AGA	GAA	TTT	CAC	TAT	ATT	CAG	AGC	AGA	CTA	GGA	ATT	
	V	S	L	L	L	G	T	I	H	A	L	I	F	A	W	N	K	W	I	D	
841	GTT	TCC	CTT	CTA	CTG	GGC	ACA	ATA	CAC	GCA	TTG	ATT	TTT	GCC	TGG	AAT	AAG	TGG	ATA	GAT	
	I	K	Q	F	V	W	Y	T	P	P	T	F	M	I	A	V	F	L	P	I	
901	ATA	AAA	CAA	TTT	GTA	TGG	TAT	ACA	CCT	CCA	ACT	TTT	ATT	ATA	GCT	GTT	TTC	CTT	CCA	ATT	
	V	V	L	I	F	K	S	I	L	F	L	P	C	L	R	K	K	I	L	K	
961	GTT	GTC	CTG	ATA</																	

FIG. 1B

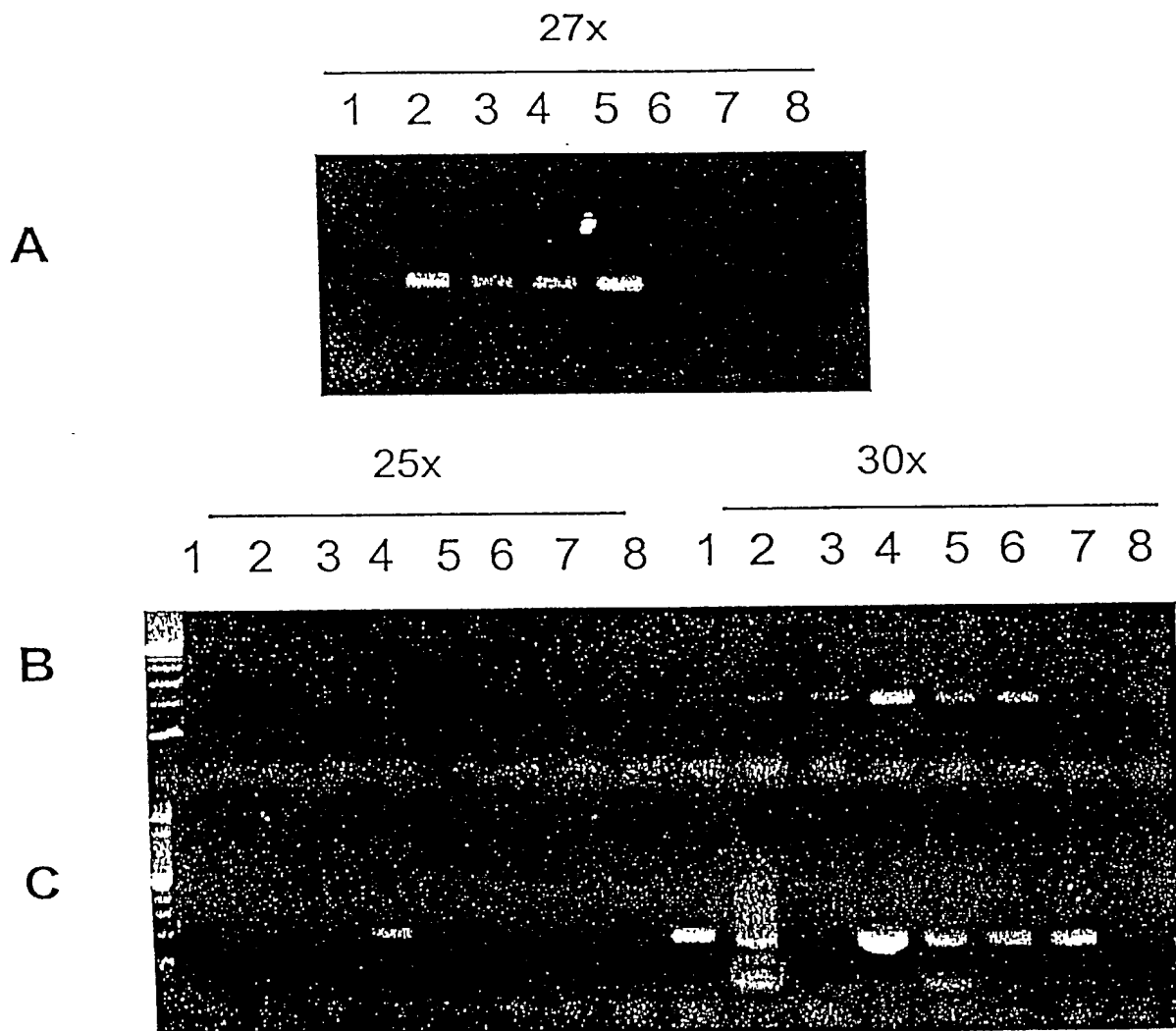


$$\frac{d^2 \phi}{dt^2} = -\frac{\partial V}{\partial \phi}, \quad \text{where } V(\phi) = \frac{1}{2} m^2 \phi^2 + \frac{\lambda}{4!} \phi^4.$$

FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GGC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3' (SEQ ID NO:3)

FIG. 2



Panels:

A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

B

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

C

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 3A

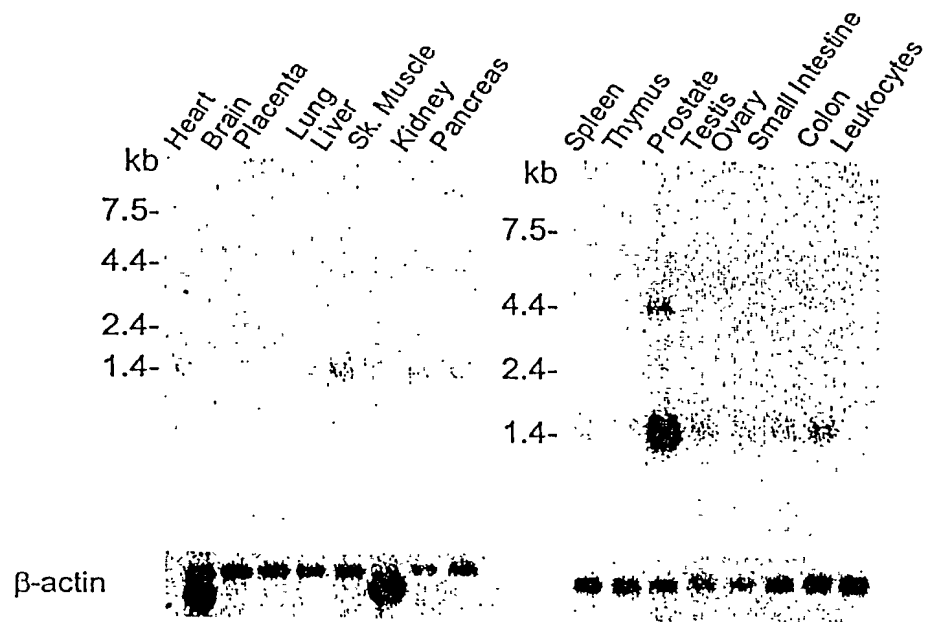


FIG. 3B

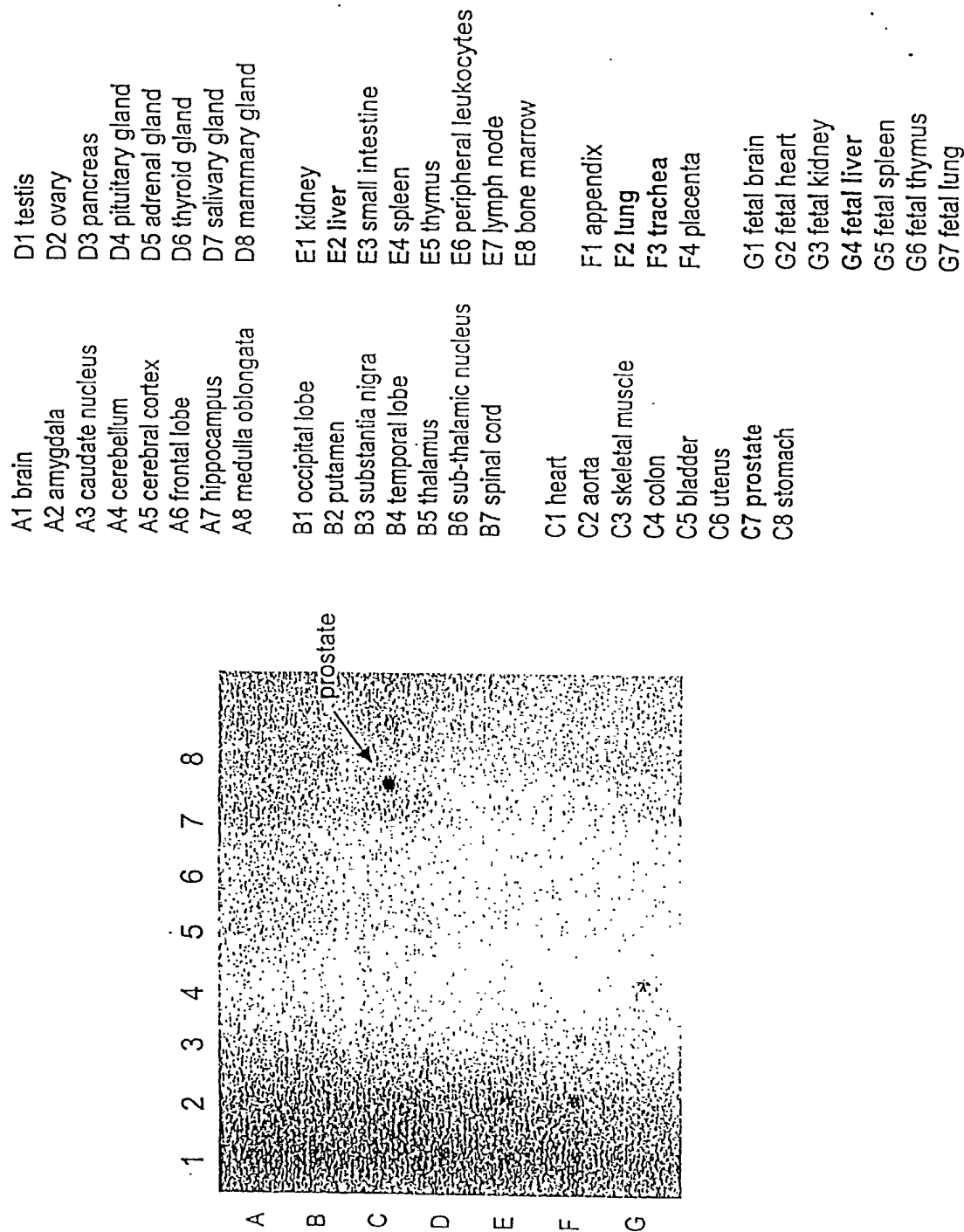


FIG. 4-1

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC
 ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG
 AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC
 ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACCTCTTCCACA
 GTGGCACTTGCCAATTAATAAGCTGCTATTATAGCATCTCTGACTTTTTCTTTACACTCTTCTGAGGGAAGTAATT
 CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCGAATCCTGGTCATCAACAAAGTCTTGCCAATGG
 TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTTCATAATGGAACCA
 GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT
 GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT
 ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT
 GGGAAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG
 AGAGAATTTCACTATATTCAGGTAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT
 ATAGAATATGTTGACTTTACCCATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTGTTCCAATT
 AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAATAAAGGCAT
 TAAAAATATTCTTTGTTTTTTTTTTTTGTTTGTGTTGTTTTGTTTGTGTTGTTTTGTTTGTGATGAAGTCTCG
 CTCTGTTGCCCATGCTGGAGTACAGTGGCAGCATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAAGCGATT
 TCTTGCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTAGTA
 GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCACCTCGGCCTCCC
 AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATTT
 GCTACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTTATTATTTCTAAAAAATATTCTTTTACC
 TGTCACTGAATTTAGTAATGCCTTTTATGTTACACAACCTTAGCACTTTCCAGAAACAAAACTCTCTCCTTGAA
 TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT
 ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT
 GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGCTGACAAGATTCAAAGGACTAA

FIG. 4-2

TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT
CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCTAATTTTGTAGGTTTACG
CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA
TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACCTGAGCCTATTCTACTATATGTACA
ATACCTAGCCATAATAGGTATACAATACACATTTGGTAAAATAATTTTCAACCAATGACATGATTTTTTCAACT
AGTAACCTAGAAATGTTTCACTTAAATCTGAGAAGTGGTTACACTACAAGTTACCTGGAGATTCATATATGAAA
ACGCAAACTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTTCGATTTGTTCT
GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT
TGAGATTACATAGGTGAACAACCTATTTTAAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA
ATGTTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTTCATATTATTTCCATGTTATC
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAAATCAGAGTGAATCA
CATTAGTCGCCTTCACAACCTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT
TTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT
GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAAATAAATATCATAAG
GGGATGAACAAAATGGTGGAGAAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG
TTCACTTAGACAGCTTGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG
TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG
ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTCTTTTGCAGAGCAAGCTAGGA
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG
TATGGTATACACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGTCCTGATATTTAAAGCATACTATT
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACCTGAG
ATATGTTCCAGTTGTAGAATTACTGTTTACACACATTTTGTTCATATTGATATATTTTATCACCACATTTCA
AGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:6)

FIG. 6

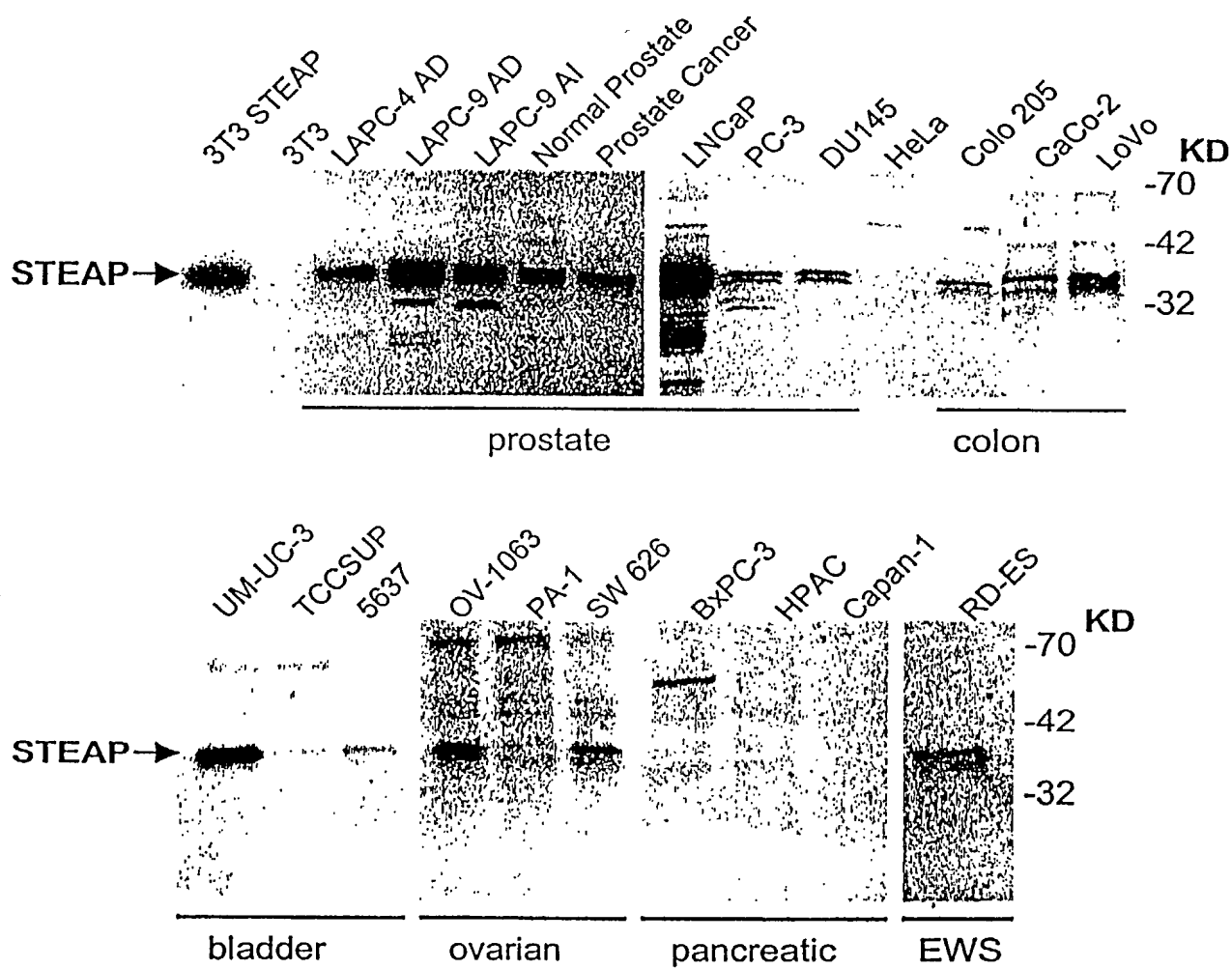
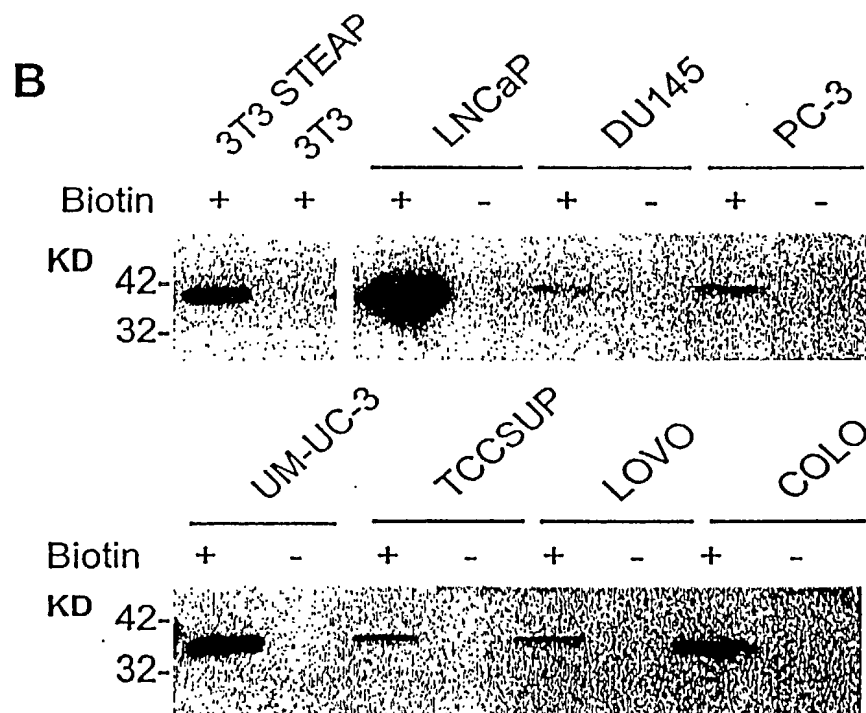
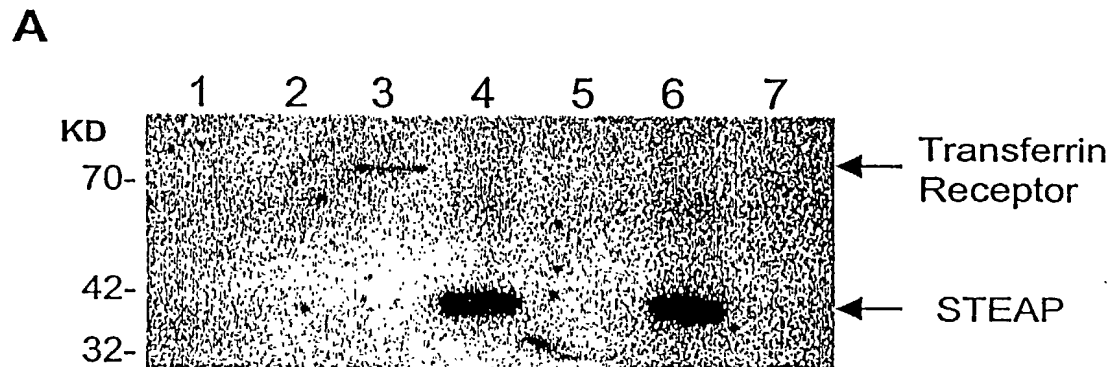


FIG. 7

• • •

5'	10			19			28			37			46			55		
	GAC	TTT	TAC	AAA	ATT	CCT	ATA	GAG	ATT	GTG	AAT	AAA	ACC	TTA	CCT	ATA	GTT	GCC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Asp	Phe	Tyr	Lys	Ile	Pro	Ile	Glu	Ile	Val	Asn	Lys	Thr	Leu	Pro	Ile	Val	Ala
		64				73			82			91			100			109
	ATT	ACT	TTG	CTC	TCC	CTA	GTA	TAC	CTC	GCA	GGT	CTT	CTG	GCA	GCT	GCT	TAT	CAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ile	Thr	Leu	Leu	Ser	Leu	Val	Tyr	Leu	Ala	Gly	Leu	Leu	Ala	Ala	Ala	Tyr	Gln
		118				127			136			145			154			163
	CTT	TAT	TAC	GGC	ACC	AAG	TAT	AGG	AGA	TTT	CCA	CCT	TGG	TTG	GAA	ACC	TGG	TTA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Tyr	Tyr	Gly	Thr	Lys	Tyr	Arg	Arg	Phe	Pro	Pro	Trp	Leu	Glu	Thr	Trp	Leu
		172				181			190			199			208			217
	CAG	TGT	AGA	AAA	CAG	CTT	GGA	TTA	CTA	AGT	TTT	TTC	TTC	GCT	ATG	GTC	CAT	GTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Gln	Cys	Arg	Lys	Gln	Leu	Gly	Leu	Leu	Ser	Phe	Phe	Phe	Ala	Met	Val	His	Val
		226				235			244			253			262			271
	GCC	TAC	AGC	CTC	TGC	TTA	CCG	ATG	AGA	AGG	TCA	GAG	AGA	TAT	TTG	TTT	CTC	AAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser	Glu	Arg	Tyr	Leu	Phe	Leu	Asn
	280				289			298			307			316			325	
ATG	GCT	TAT	CAG	CAG	GTT	CAT	GCA	AAT	ATT	GAA	AAC	TCT	TGG	AAT	GAG	GAA	GAA	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
Met	Ala	Tyr	Gln	Gln	Val	His	Ala	Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu	
	334				343			352			361			370			379	
GTT	TGG	AGA	ATT	GAA	ATG	TAT	ATC	TCC	TTT	GGC	ATA	ATG	AGC	CTT	GGC	TTA	CTT	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
Val	Trp	Arg	Ile	Glu	Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu	
	388				397			406			415			424			433	
TCC	CTC	CTG	GCA	GTC	ACT	TCT	ATC	CCT	TCA	GTG	AGC	AAT	GCT	TTA	AAC	TGG	AGA	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
Ser	Leu	Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp	Arg	
	442				451			460			469			478			487	
GAA	TTC	AGT	TTT	ATT	CAG	TCT	ACA	CTT	GGA	TAT	GTC	GCT	CTG	CTC	ATA	AGT	ACT	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu	Leu	Ile	Ser	Thr	
	496				505			514										
TTC	CAT	GTT	TTA	ATT	TAT	GGA	TGG	AAA	CGA	GCT	3' (SEQ ID NO:7)							
---	---	---	---	---	---	---	---	---	---	---								
Phe	His	Val	Leu	Ile	Tyr	Gly	Trp	Lys	Arg	Ala	(SEQ ID NO:8)							

FIG. 10

STEAP-2, AA508880 (NCI_CGAP Pr6)

ggtcgacttttcctttattcctttgtcagagatctgattcatccatatgctagaaaccaacagagtgacttttaca
aaattcctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctagtataccttgcagg
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttgggtggaaacctgggtta
cagtgtagaaaacagcttggattactaagttgtttcttcgctatgggtccatgttgctacagcctctgcttacga
tgagaaggtcagagagat (SEQ ID NO:9)

STEAP-2, 98P4B6 SSH fragment

TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAACCTGGAATTTGTCTTCCTATTGACTCTACTTCTTTAAAAGCG
GCTGCCCATTAATTCCCTCAGCTGTCCTTGCAAGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGTCCTTTT (SEQ ID NO:10)

AI139607 (testis EST)

aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaataacttggggtttt
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcgaactggagagagttccgatttgt
ccagtcctaaactgggttatttgacctgatcttgtgtacagccacacccctgggtgtacgggtgggaagagattcctc
agcccttcaaactcagatgggtatcttctcagcctacgtgttaggggttatcatctccttgactgtggtgga
tcaagtttgtcctaatacatgccatgtgtagacaacacccttacaaggatccgcccagggtgggaaagggaactcaaa
acactagaaaaagcattgaatggaaaatcaatatttaaaacaaagttcaatttagctggaaaaaaa (SEQ ID NO:11)

R80991 (placental EST)

ggccgcggcanccgctacgacctgggtcaacctggcagtcgaagcaggtcttggccanacaagagccacctctgggtg
aaggaggaggtctggcggatggagatctacctctccctgggagtgctggccctcggcagcttgtccctgctggccg
tgacctcactgccgtccattgcaaaactcgctcaactggaggagttcagcttcgttcagtcctcactgggctttgt
ggcctcgtgctgagcacactncacacgctcacctacgggtggaccgcgccttcgaggagagccgctacaagttc
tacctnctcccaccttcacgntcacgctgctgggtgccctgcgttcggttcacctcctgggccaagccctggttntac
tgcttgcattcagccgnaga (SEQ ID NO:12)

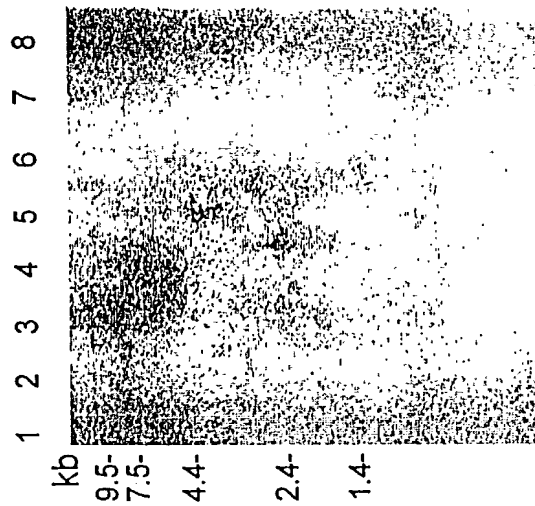
FIG. 11A

STEAP-1	106	FYKIPILVINKVLPV SITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFG
STEAP-2	2	FYKIPIEIVNKTLP IVAITLLSLVYLAGLLAAAYQLYYGTYRRFPFWLETWLQCRKQLG
		***** * * * * * * * * * * * * * * *
STEAP-1	166	LLSFFFAVLHAIYSLSPMRRSYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIV
STEAP-2	62	LLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIM
		***** * * * * * * * * * * * * * *
		(Portion of SEQ ID NO:2)
		↓
STEAP-1	226	GLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLGTIHALIFAWN
STEAP-2	122	SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR
		* * ***** * ***** * * * * * * * * *
		(Portion of SEQ ID NO:8)
		↑

[illegible]

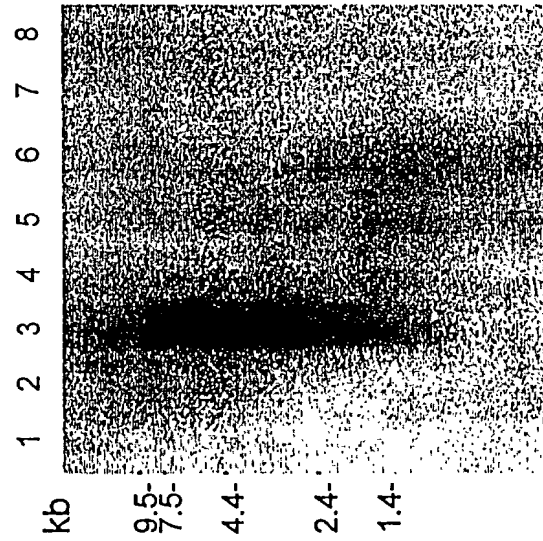
	1	15	16	30	31	45	46	60	61	75	76	
STEAP-1	MESRDIITNQEEAK	MCPRRNLEEDDYLHK	DYGETSMLKRPVLLH	LHQTAHADEFDCPSE	LQHTQELFPQWHLP	KIAAIIASLFLYTL						90
STEAP-2	---	---	---	---	---	---	---	---	---	---	---	0
STEAP-3	---	---	---	---	---	---	---	---	---	---	---	0
STEAP-4	---	---	---	---	---	---	---	---	---	---	---	0
STEAP-1	LREVIHPLATSEQQ	FYKIPILVINKVLP	NSITLLALVYLP	GVV	AAIVQLHNGTKYKGF	PHWLLKMWLTKRQFG	LLSFFFPVNLHAIYST					180
STEAP-2	---	---	---	---	---	---	---	---	---	---	---	76
STEAP-3	---	---	---	---	---	---	---	---	---	---	---	0
STEAP-4	---	---	---	---	---	---	---	---	---	---	---	0
STEAP-1	SYEMRPSVRYKELM	AYQOQVQNKEDAWIE	HDVWRMEIYVSLGIV	GLAIIALLAVTSIPS	VSDSLTWREFFHYIQS	KLGIIVSLLGLTTHAL						270
STEAP-2	CLPMRPSERYLEAM	AYQOQVHANTENSWE	ESVWRIEMVTSFGIM	SLGLLSLLAVTSIPS	VSNALNWRESSTIQS	TLGYVALLISTPHTL						166
STEAP-3	---	---	---	---	---	---	---	---	---	---	---	68
STEAP-4	---	---	---	---	---	---	---	---	---	---	---	82
STEAP-1	IFAMAKWIDIKQFVW	YTPPTFNIAVLP	VLIFKSIPLFLPCTLRK	KILKIRHGWEDVTKI	NKTEICSQL	339 (SEQ ID NO:2)						360
STEAP-2	ITYGWRGA	---	---	---	---	---						173 (SEQ ID NO:8)
STEAP-3	YVGGKFLSPSKLRW	YLPAAVVLGLIIPCT	VLVIKFLVILPCVDN	TLTRIRQGEERNKSH	---	---						128 (Portion of SEQ ID NO:2)
STEAP-4	TYGWTAFEEESIKF	YLPPTFTYTLVLVPCV	RSSWAKALFXLP	CIQ P	---	---						128 (Portion of SEQ ID NO:8)

FIG. 15A



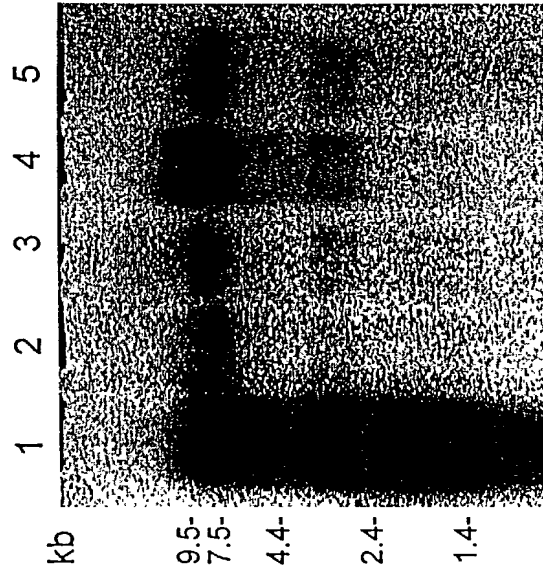
1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas

FIG. 15B



1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Ovary
6. Small Intestine
7. Colon
8. Leukocytes

FIG. 15C



1. Prostate
2. LAPC-4 AD
3. LAPC-4 AI
4. LAPC-9 AD
5. LAPC-9 AI

FIG. 16

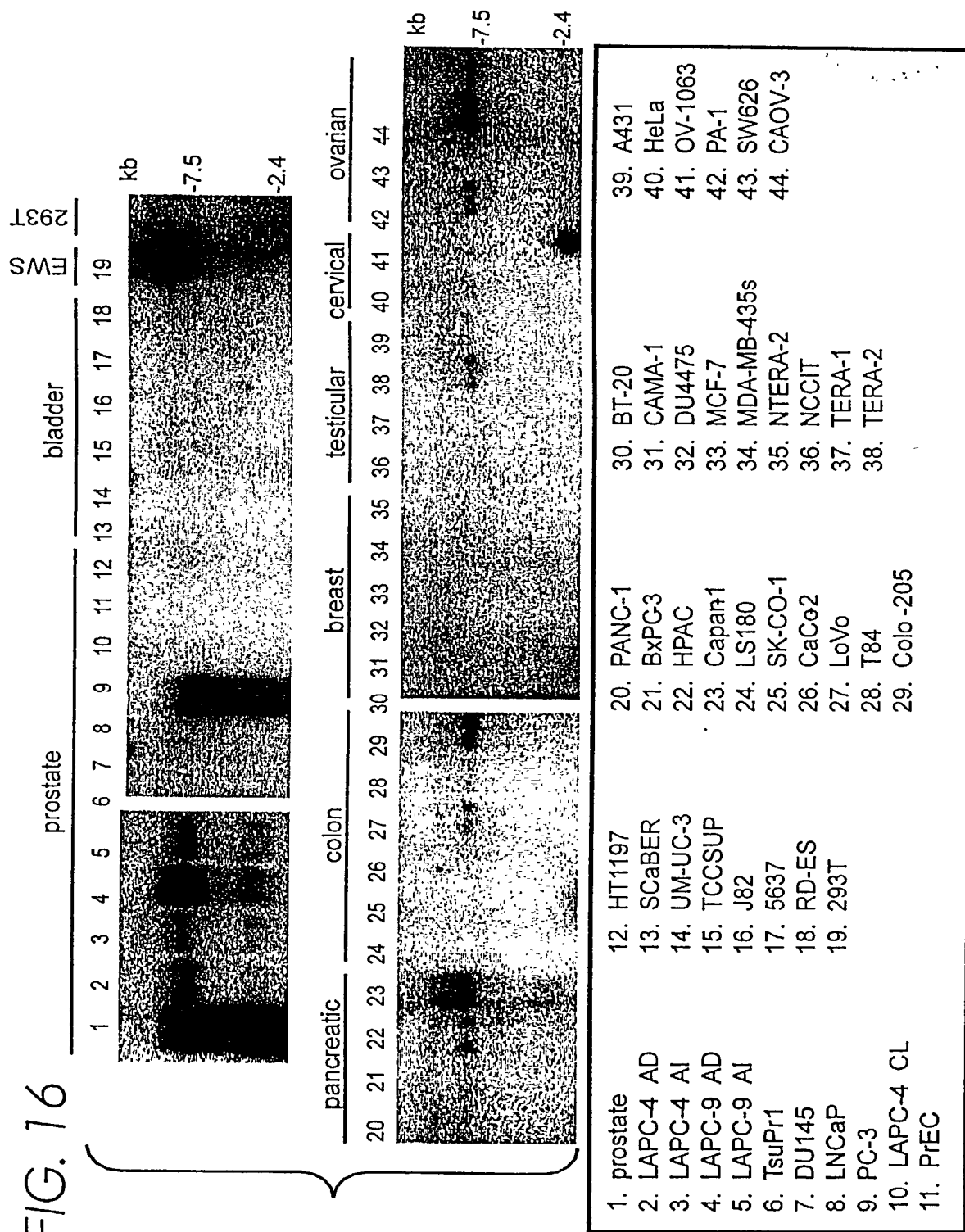


FIG. 17

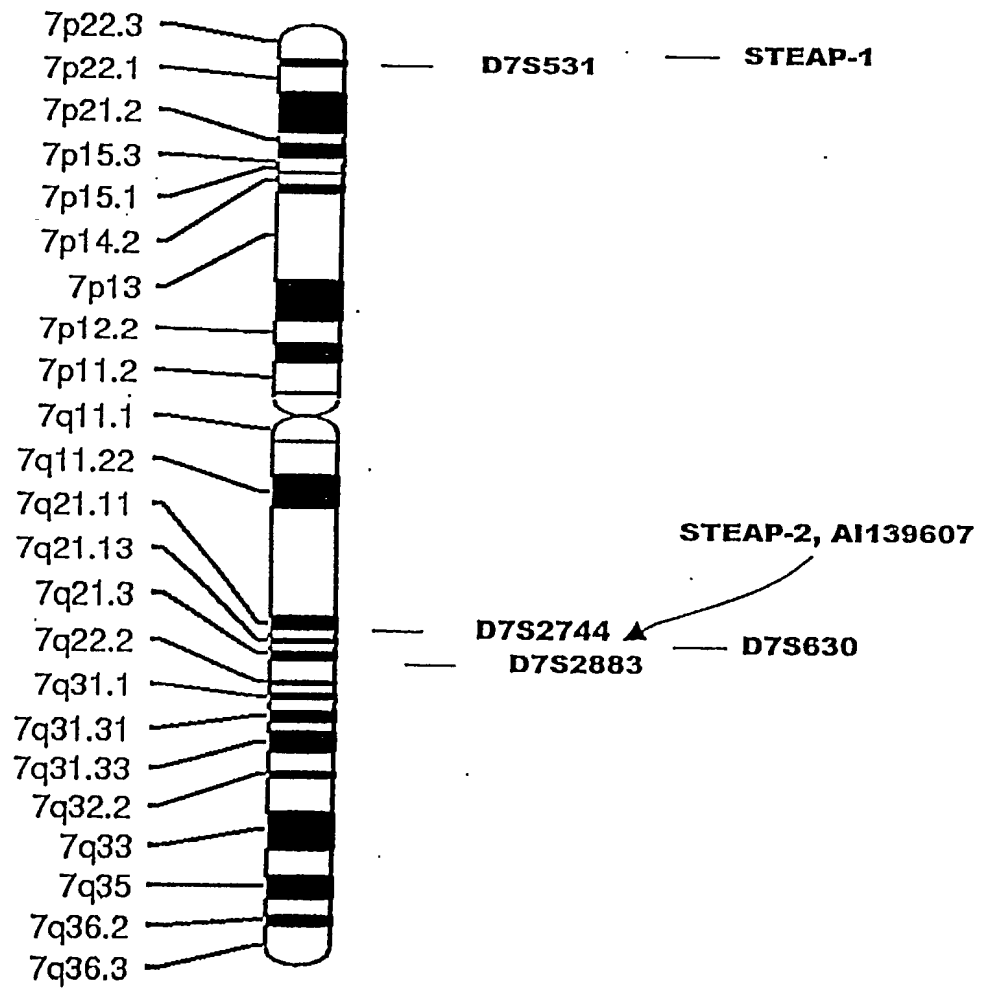


FIG. 19

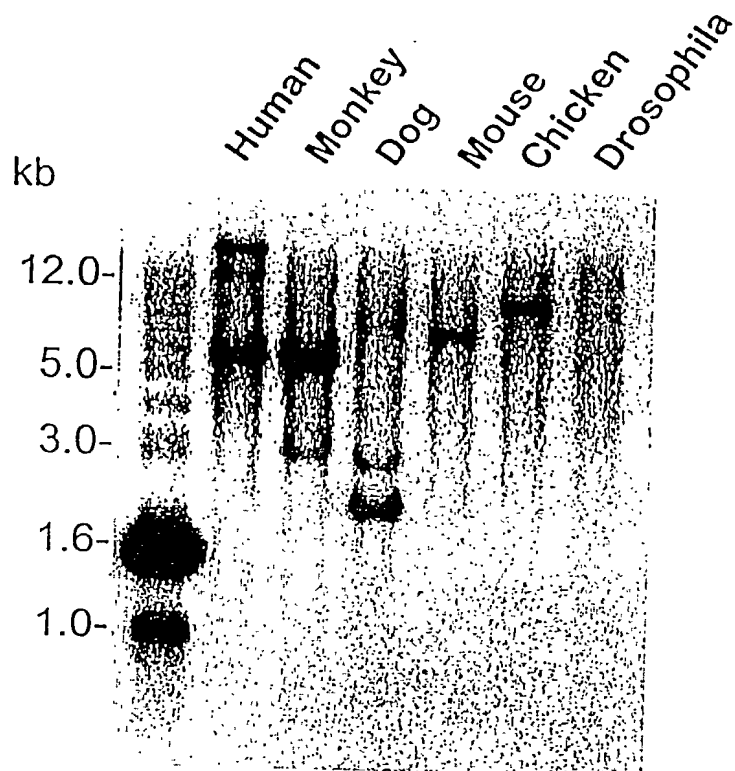
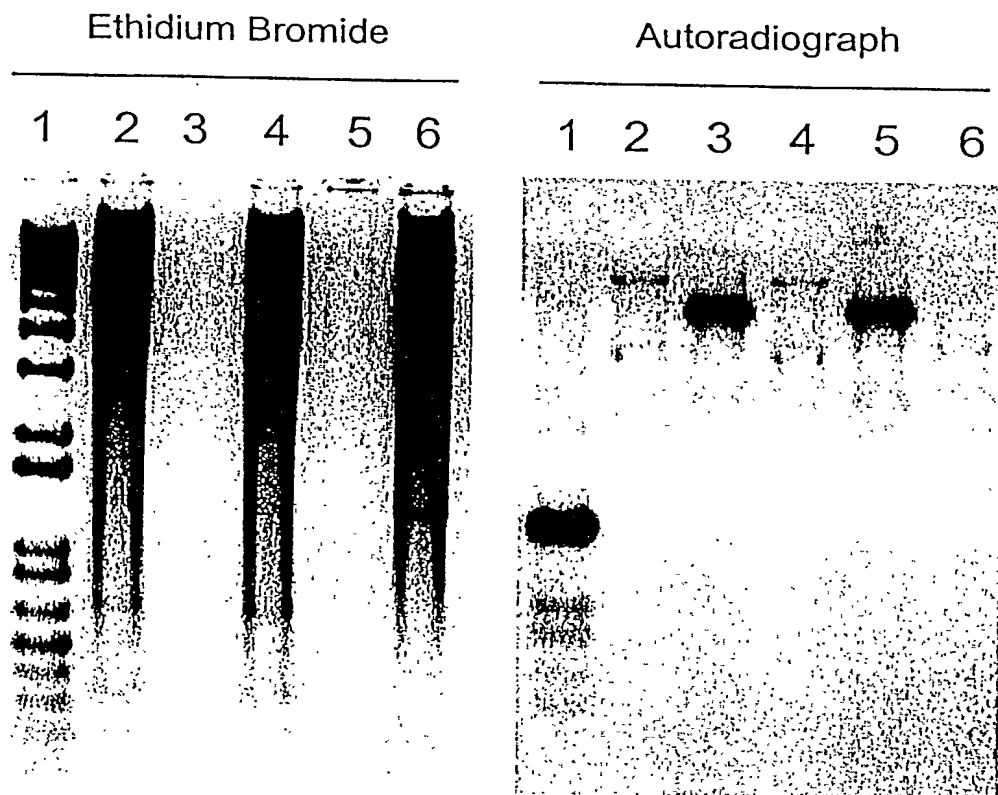


FIG. 20**Lanes**

- 1) 1kb ladder
- 2) human female genomic
- 3) 12P11 BAC mus
- 4) human female genomic
- 5) 12P11 BAC mus
- 6) 3T3